

1648

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/407,432

DATE: 02/20/2001  
 TIME: 15:04:25

Input Set : A:\548581.app  
 Output Set: N:\CRF3\02202001\I407432.raw

RECEIVED  
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 TECH CENTER 1600/2500  
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3 <110> APPLICANT: Worman, Howard J.  
 4 Mamiya, Naoto  
 6 <120> TITLE OF INVENTION: HCV CORE PROTEIN BINDING AGENTS FOR TREATMENT OF  
 7 HEPATITIS C VIRUS INFECTION  
 9 <130> FILE REFERENCE: 0575/54858  
 11 <140> CURRENT APPLICATION NUMBER: 09/407,432  
 12 <141> CURRENT FILING DATE: 1999-09-29  
 14 <160> NUMBER OF SEQ ID NOS: 6  
 16 <170> SOFTWARE: PatentIn Ver. 2.1  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 666  
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 28 20 25 30  
 30 Ala Ser Lys Gly Arg Tyr Ile Pro Pro His Leu Arg Asn Arg Glu Ala  
 31 35 40 45  
 33 Thr Arg Gly Phe Tyr Asp Lys Asp Ser Ser Gly Trp Ser Ser Ser Lys  
 34 50 55 60  
 36 Asp Lys Asp Ala Tyr Ser Phe Gly Ser Arg Ser Asp Ser Arg Gly  
 37 65 70 75 80  
 39 Lys Ser Ser Phe Phe Ser Asp Arg Gly Ser Gly Ser Arg Gly Arg Phe  
 40 85 90 95  
 42 Phe Asp Asp Arg Gly Arg Ser Asp Tyr Asp Gly Ile Gly Ser Arg Gly  
 43 100 105 110  
 45 Asp Arg Ser Gly Arg Gly Lys Phe Glu Arg Gly Gly Asn Ser Arg Trp  
 46 115 120 125  
 48 Cys Asp Lys Ser Asp Glu Asp Asp Trp Ser Lys Pro Leu Pro Pro Ser  
 49 130 135 140  
 51 Glu Arg Leu Glu Gln Glu Leu Phe Ser Gly Gly Asn Thr Gly Ile Asn  
 52 145 150 155 160  
 54 Phe Glu Lys Tyr Asp Asp Ile Pro Val Glu Ala Thr Gly Asn Asn Cys  
 55 165 170 175  
 57 Pro Pro His Ile Glu Ser Phe Ser Asp Val Val Val Glu Met Gly Glu  
 58 180 185 190  
 60 Ile Ile Met Gly Asn Ile Glu Leu Thr Arg Tyr Thr Arg Pro Thr Pro  
 61 195 200 205  
 63 Val Gln Lys His Ala Ile Pro Ile Ile Lys Glu Lys Arg Asp Leu Met  
 64 210 215 220  
 66 Ala Cys Ala Gln Thr Gly Ser Gly Lys Thr Ala Ala Phe Leu Leu Pro  
 67 225 230 235 240  
 69 Ile Leu Ser Gln Ile Tyr Ser Asp Gly Pro Gly Glu Ala Leu Arg Ala  
 70 245 250 255  
 72 Met Lys Glu Asn Gly Arg Tyr Gly Arg Arg Lys Gln Tyr Pro Ile Ser

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73          260          265          270
75 Leu Val Leu Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Tyr Glu Glu
76          275          280          285
78 Ala Arg Lys Phe Ser Tyr Arg Ser Arg Val Arg Pro Cys Val Val Tyr
79          290          295          300
81 Gly Gly Ala Asp Ile Gly Gln Gln Ile Arg Asp Leu Glu Arg Gly Cys
82 305          310          315          320
84 His Leu Leu Val Ala Thr Pro Gly Arg Leu Val Asp Met Met Glu Arg
85          325          330          335
87 Gly Lys Ile Gly Leu Asp Phe Cys Lys Tyr Leu Val Leu Asp Glu Ala
88          340          345          350
90 Asp Arg Met Leu Asp Met Gly Phe Glu Pro Gln Ile Arg Arg Ile Val
91          355          360          365
93 Glu Gln Asp Thr Met Pro Pro Lys Gly Val Arg His Thr Met Met Phe
94          370          375          380
96 Ser Ala Thr Phe Pro Lys Glu Ile Gln Met Leu Ala Arg Asp Phe Leu
97 385          390          395          400
99 Asp Glu Tyr Ile Phe Leu Ala Val Gly Arg Val Gly Ser Thr Ser Glu
100          405          410          415
102 Asn Ile Thr Gln Lys Val Val Trp Val Glu Glu Ser Asp Lys Arg Ser
103          420          425          430
105 Phe Leu Leu Asp Leu Leu Asn Ala Thr Gly Lys Asp Ser Leu Thr Leu
106          435          440          445
108 Val Phe Val Glu Thr Lys Lys Gly Ala Asp Ser Leu Glu Asp Phe Leu
109          450          455          460
111 Tyr His Glu Gly Tyr Ala Cys Thr Ser Ile His Gly Asp Arg Ser Gln
112 465          470          475          480
114 Arg Asp Arg Glu Glu Ala Leu His Gln Phe Arg Ser Gly Lys Ser Pro
115          485          490          495
117 Ile Leu Val Ala Thr Ala Val Ala Ala Arg Gly Leu Asp Ile Ser Asn
118          500          505          510
120 Val Lys His Val Ile Asn Phe Asp Leu Ser Pro Ser Asp Ile Glu Glu
121          515          520          525
123 Tyr Val His Arg Ile Gly Arg Thr Gly Arg Val Gly Asn Leu Gly Leu
124          530          535          540
126 Ala Thr Ser Phe Phe Asn Glu Arg Asn Ile Asn Ile Thr Lys Asp Leu
127 545          550          555          560
129 Leu Asp Leu Leu Val Glu Ala Lys Gln Glu Val Pro Ser Trp Leu Glu
130          565          570          575
132 Asn Met Ala Tyr Glu His His Tyr Lys Gly Ser Ser Arg Gly Arg Ser
133          580          585          590
135 Lys Ser Ser Arg Phe Ser Gly Gly Phe Gly Ala Arg Asp Tyr Arg Gln
136          595          600          605
138 Ser Ser Gly Ala Ser Ser Ser Ser Phe Ser Ser Ser Arg Ala Ser Ser
139          610          615          620
141 Ser Arg Ser Gly Gly Gly Gly His Gly Ser Ser Arg Gly Phe Gly Gly
142 625          630          635          640
144 Gly Gly Tyr Gly Gly Phe Tyr Asn Ser Asp Gly Tyr Gly Gly Asn Tyr
145          645          650          655

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152 <211> LENGTH: 254
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154 <213> ORGANISM: Human
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160 Ser Asp Lys Arg Ser Phe Leu Leu Asp Leu Leu Asn Ala Thr Gly Lys
161           20           25           30
163 Asp Ser Leu Thr Leu Val Phe Val Glu Thr Lys Lys Gly Ala Asp Ser
164           35           40           45
166 Leu Glu Asp Phe Leu Tyr His Glu Gly Tyr Ala Cys Thr Ser Ile His
167           50           55           60
169 Gly Asp Arg Ser Gln Arg Asp Arg Glu Glu Ala Leu His Gln Phe Arg
170   65           70           75           80
172 Ser Gly Lys Ser Pro Ile Leu Val Ala Thr Ala Val Ala Ala Arg Gly
173           85           90           95
175 Leu Asp Ile Ser Asn Val Lys His Val Ile Asn Phe Asp Leu Pro Ser
176           100          105          110
178 Asp Ile Glu Tyr Val His Arg Ile Gly Arg Thr Gly Arg Val Gly
179           115          120          125
181 Asn Leu Gly Leu Ala Thr Ser Phe Phe Asn Glu Arg Asn Ile Asn Ile
182   130          135          140
184 Thr Lys Asp Leu Leu Asp Leu Leu Val Glu Ala Lys Gln Glu Val Pro
185 145          150          155          160
187 Ser Trp Leu Glu Asn Met Ala Tyr Glu His His Tyr Lys Gly Ser Ser
188           165          170          175
190 Arg Gly Arg Ser Lys Ser Ser Arg Phe Ser Gly Gly Phe Gly Ala Arg
191           180          185          190
193 Asp Tyr Arg Gln Ser Ser Gly Ala Ser Ser Ser Ser Phe Ser Ser Ser
194           195          200          205
196 Arg Ala Ser Ser Ser Arg Ser Gly Gly Gly Gly His Gly Ser Ser Arg
197           210          215          220
199 Gly Phe Gly Gly Gly Gly Tyr Gly Gly Phe Tyr Asn Ser Asp Gly Tyr
200 225          230          235          240
202 Gly Gly Asn Tyr Asn Ser Gln Gly Val Asp Trp Trp Gly Asn
203           245          250
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 136
208 <212> TYPE: PRT
209 <213> ORGANISM: Human
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213   1           5           10           15
215 Glu Ser Asp Lys Arg Ser Phe Leu Leu Asp Leu Leu Asn Ala Thr Gly
216           20           25           30
218 Lys Asp Ser Leu Thr Leu Val Phe Val Glu Thr Lys Lys Gly Ala Asp

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219          35          40          45
221 Ser Leu Glu Asp Phe Leu Tyr His Glu Gly Tyr Ala Cys Thr Ser Ile
222          50          55          60
224 His Gly Asp Arg Ser Gln Arg Asp Arg Glu Glu Ala Leu His Gln Phe
225 65          70          75          80
227 Arg Ser Gly Lys Ser Pro Ile Leu Val Ala Thr Ala Val Val Ala Ala
228          85          90          95
230 Arg Gly Leu Asp Ile Ser Asn Val Lys His Val Ile Asn Phe Asp Leu
231          100          105          110
233 Pro Ser Asp Ile Glu Glu Tyr Val His Arg Ile Gly Arg Thr Gly Arg
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245 <220> FEATURE:
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (1)..(765)
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251 Met Asp Asp Arg Glu Asp Leu Val Tyr Gln Ala Lys Leu Ala Glu Gln
252 1 5 10 15
254 gct gag cga tac gac gaa atg gtg gag tca atg aag aaa gta gca ggg 96
255 Ala Glu Arg Tyr Asp Glu Met Val Glu Ser Met Lys Lys Val Ala Gly
256 20 25 30
258 atg gat gtg gag ctg aca gtt gaa gaa aga aac ctc cta tct gtt gca 144
259 Met Asp Val Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala
260 35 40 45
262 tat aag aat gtg att gga gct aga aga gcc tcc tgg aga ata atc agc 192
263 Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser
264 50 55 60
266 agc att gaa cag aaa gaa gaa aac aag gga gga gaa gac aag cta aaa 240
267 Ser Ile Glu Gln Lys Glu Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys
268 65 70 75 80
270 atg att cgg gaa tat cgg caa atg gtt gag act gag cta aag tta atc 288
271 Met Ile Arg Glu Tyr Arg Gln Met Val Glu Thr Glu Leu Lys Leu Ile
272 85 90 95
274 tgt tgt gac att ctg gat gta ctg gac aaa cac ctc att cca gca gct 336
275 Cys Cys Asp Ile Leu Asp Val Leu Asp Lys His Leu Ile Pro Ala Ala
276 100 105 110
278 aac act ggc gag tcc aag gtt ttc tat tat aaa atg aaa ggg gac tac 384
279 Asn Thr Gly Glu Ser Lys Val Phe Tyr Tyr Lys Met Lys Gly Asp Tyr
280 115 120 125
282 cac agg tat ctg gca gaa ttt gcc aca gga aac gac agg aag gag gct 432
283 His Arg Tyr Leu Ala Glu Phe Ala Thr Gly Asn Asp Arg Lys Glu Ala
284 130 135 140
286 gcg gag aac agc cta gtg gct tat aaa gct gct agt gat att gca atg 480

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287 Ala Glu Asn Ser Leu Val Ala Tyr Lys Ala Ala Ser Asp Ile Ala Met
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290 aca gaa ctt cca cca acg cat cct att cgc tta ggt ctt gct ctc aat 528
291 Thr Glu Leu Pro Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn
292      165      170      175
294 ttt tcc gta ttc tac tac gaa att ctt aat tcc cct gac cgt gcc tgc 576
295 Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Asp Arg Ala Cys
296      180      185      190
298 agg ttg gca aaa gca gct ttt gat gat gca att gca gaa ctg gat acg 624
299 Arg Leu Ala Lys Ala Ala Phe Asp Asp Ala Ile Ala Glu Leu Asp Thr
300      195      200      205
302 ctg agt gaa gaa agc tat aag gac tct aca ctt atc atg cag ttg tta 672
303 Leu Ser Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu
304      210      215      220
306 cgt gat aat ctg aca cta tgg act tca gac atg cag ggt gac ggt gaa 720
307 Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Gly Asp Gly Glu
308 225      230      235      240
310 gag cag aat aaa gaa gcg ctg cag gac gtg gaa gac gaa aat cag 765
311 Glu Gln Asn Lys Glu Ala Leu Gln Asp Val Glu Asp Glu Asn Gln
312      245      250      255
314 tgagacataa gccacaaga gaaacca 792
317 <210> SEQ ID NO: 5
318 <211> LENGTH: 255
319 <212> TYPE: PRT
320 <213> ORGANISM: Human
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326 Ala Glu Arg Tyr Asp Glu Met Val Glu Ser Met Lys Lys Val Ala Gly
327      20      25      30
329 Met Asp Val Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala
330      35      40      45
332 Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser
333      50      55      60
335 Ser Ile Glu Gln Lys Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys
336 65      70      75      80
338 Met Ile Arg Glu Tyr Arg Gln Met Val Glu Thr Glu Leu Lys Leu Ile
339      85      90      95
341 Cys Cys Asp Ile Leu Asp Val Leu Asp Lys His Leu Ile Pro Ala Ala
342      100      105      110
344 Asn Thr Gly Glu Ser Lys Val Phe Tyr Tyr Lys Met Lys Gly Asp Tyr
345      115      120      125
347 His Arg Tyr Leu Ala Glu Phe Ala Thr Gly Asn Asp Arg Lys Glu Ala
348      130      135      140
350 Ala Glu Asn Ser Leu Val Ala Tyr Lys Ala Ala Ser Asp Ile Ala Met
351 145      150      155      160
353 Thr Glu Leu Pro Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn
354      165      170      175
356 Phe Ser Val Phe Tyr Glu Ile Leu Asn Ser Pro Asp Arg Ala Cys

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VERIFICATION SUMMARY                      DATE: 02/20/2001  
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Input Set : A:\548581.app  
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